

SEQUENCE LISTING

<110> Sharpe, Arlene H.
 Borriello, Francescopaulo
 Freeman, Gordon J.
 Nadler, Lee M.

<120> B7 Domain-Specific Antibodies

<130> BWI-120CPADV2

<140> 09/837,867

<141> 2001-04-17

<150> 08/205,697

<151> 1994-03-02

<160> 42

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1888

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(1208)

<400> 1

```

gagttttata cctcaataga ctcttactag tttctctttt tcaggttggtg aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
tggaatgccat ccaggcttct tttctacat ctctgttctt cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
          1              5              10

```

```

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
  15              20              25              30

```

```

ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
          35              40              45

```

```

aaa gat aag gta ttg ctg cct tgc cgt tac aac tct cct cat gaa gat 434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
          50              55              60

```

```

gag tct gaa gac cga atc tac tgg caa aaa cat gac aaa gtg gtg ctg 482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
          65              70              75

```

```

tct gtc att gct ggg aaa cta aaa gtg tgg ccc gag tat aag aac cgg 530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
          80              85              90

```

```

act tta tat gac aac act acc tac tct ctt atc atc ctg ggc ctg gtc 578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val

```

95	100	105	110	
ctt tca gac cgg ggc aca tac agc tgt gtc gtt caa aag aag gaa aga				626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	115	120	125	
gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa				674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	130	135	140	
gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca				722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	145	150	155	
gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct				770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	160	165	170	
cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg				818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	175	180	185	190
aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa				866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	195	200	205	
cta gat ttc aat acg act cgc aac cac acc att aag tgt ctc att aaa				914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	210	215	220	
tat gga gat gct cac gtg tca gag gac ttc acc tgg gaa aaa ccc cca				962
Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	225	230	235	
gaa gac cct cct gat agc aag aac aca ctt gtg ctc ttt ggg gca gga				1010
Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	240	245	250	
ttc ggc gca gta ata aca gtc gtc gtc atc gtt gtc atc atc aaa tgc				1058
Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	255	260	265	270
ttc tgt aag cac ggt ctc atc tac cat ttg caa ctg acc tct tct gca				1106
Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala	275	280	285	
aag gac ttc aga aac cta gca cta ccc tgg ctc tgc aaa cac ggt tct				1154
Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser	290	295	300	
cta ggt gaa gcc tct gca gtg att tgc aga agt act cag acg aat gaa				1202
Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu	305	310	315	
cca cag tagttctgct gtttctgagg acgtagttaa gagactgaat tctttggaaa				1258
Pro Gln	320			
ggacataggg acagtttgca catttgcttg cacatcacac acacacacac acacacacac				1318
acacacacac acacacacac acacacacac acacacacac tctctctctc tctctctctc				1378
gataccttag gatagggttc taccctgttg ctgagtgaca aagaatcact ctgtggcgga				1438

```

ggcaggcttc aagcttgacg caatcctcct gcaccagttt cctgagtgcc agacttccag 1498
gtgtaagcta tggcacttag cagaacacta gctgaatcaa tgaagacact gaggttccaa 1558
gagggaaacct gaattatgaa ggtgagtcag aatccagatt tcctggctct accactctta 1618
acctgtatct gttagacccc aagctctgag ctcatagaca agctaattta aaatgctttt 1678
taataagcag aaggctcagt tagtacgggg ttcaggatac tgcttactgg caatatttga 1738
ctagcctcta ttttgtttgt tttttaaagg cctactgact gtagtgtaat ttgtaggaaa 1798
catgttgcta tgtataccca tttgagggta ataaaaatgt tggtaatattt cagccagcac 1858
tttcaggta tttccctttt tatccttcat                                     1888

```

<210> 2

<211> 320

<212> PRT

<213> Mus musculus

<400> 2

```

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1          5          10          15
Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
          20          25          30
Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
          35          40          45
Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
          50          55          60
Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
65          70          75          80
Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
          85          90          95
Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
          100          105          110
Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
          115          120          125
Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
          130          135          140
Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
145          150          155          160
Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
          165          170          175
Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
          180          185          190
Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
          195          200          205
Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
          210          215          220
Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225          230          235          240
Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
          245          250          255
Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
          260          265          270
Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp
          275          280          285
Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly
          290          295          300
Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
305          310          315          320

```

<210> 3

<211> 2516

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(1166)

<400> 3

```

gagttttata cctcaataga ctcttactag tttctctttt tcaggttgtg aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
tggatgccat ccaggcttct ttttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
          1             5             10

```

```

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg aat cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Asn Arg
  15             20             25             30

```

```

ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
          35             40             45

```

```

aaa gat aag gta ttg ctg cct tgc cgt tac aac tct cct cat gaa gat 434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
          50             55             60

```

```

gag tct gaa gac cga atc tac tgg caa aaa cat gac aaa gtg gtg ctg 482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
          65             70             75

```

```

tct gtc att gct ggg aaa cta aaa gtg tgg ccc gag tat aag aac cgg 530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
          80             85             90

```

```

act tta tat gac aac act acc tac tct ctt atc atc ctg ggc ctg gtc 578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
          95             100             105             110

```

```

ctt tca gac cgg ggc aca tac agc tgt gtc gtt caa aag aag gaa aga 626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
          115             120             125

```

```

gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa 674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
          130             135             140

```

```

gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca 722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
          145             150             155

```

```

gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct 770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
          160             165             170

```

```

cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg 818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
          175             180             185             190

```

```

aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa 866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
          195             200             205

```

gctcatgagc	tacaatcttt	ctttcagcac	cgtgctagct	gatctttcgg	acaacttgac	1266
acaagataga	gttaactggg	aagagaaagc	cttgaatgag	gatttctttc	catcaggaag	1326
ctacgggcaa	gtttgctggg	cctttgattg	cttgatgact	gaagtggaaa	ggctgagccc	1386
actgtgggtg	gtgctagccc	tgggcagggg	caggtgaccc	tgggtggtat	aagaaaaaga	1446
gctgtcacta	aaaggagagc	tgcctagtct	tactgcaact	tgatattgtc	tgttttggtt	1506
gtgtctgtgg	gaggcctgcc	cttttctgaa	gagaagtggt	gggagagtgg	atggggtggg	1566
ggcagagaaa	aagtggggga	gaggcctgg	gaggagagga	gggaggggga	cggggtgggg	1626
gtggggaaaa	ctatggttgg	gatgtaaaaa	cggataataa	tataaatatt	aaataaaaaa	1686
agagtattga	gcggtctcat	ctaccatttg	caactgacct	cttctgcaaa	ggacttcaga	1746
aacctagcac	taccctggct	ctgcaaacac	ggttctctag	gtgaagcctc	tgcagtgatt	1806
tgcagaagta	ctcagacgaa	tgaaccacag	tagttctgct	gtttctgagg	acgtagttta	1866
gagactgaat	tctttggaaa	ggacataggg	acagtttgca	catttgcttg	cacatcacac	1926
acacacacac	acacacacac	acacacacac	acacacacac	acacacacac	acacacacac	1986
tctctctctc	tctctctctc	gataccttag	cataggggtc	tacctgtgtg	ctcagtgaca	2046
aagaatcact	ctgtggcgga	ggcaggcttc	aagcttgcag	caatcctcct	gcaccagttt	2106
cctgagtgcc	agacttccag	gtgtaagcta	tggcaactag	cagaacacta	gctgaatcaa	2166
tgaagacact	gaggttccaa	gagggaaact	gaattatgaa	ggtgagtcag	aatccagatt	2226
tcttggtctc	accactctta	acctgtatct	gttagacccc	aagctctgag	ctcatagaca	2286
agctaattta	aaatgctttt	taataagcag	aaggctcagt	tagtacgggg	ttcaggatac	2346
tgcttactgg	caatatttga	ctagcctcta	ttttgtttgt	tttttaaagg	cctactgact	2406
gtagtgtaat	tgttaggaaa	catgttgcta	tgtataccca	ttttgaggga	ataaaaaatgt	2466
tggtaatttt	caqccaqcac	tttccaqgta	tttccctttt	tatccttcac		2516

```
<220>
<221> CDS
<222> (1)...(138)
```

<400> 4

ggt ctc atc tac cat ttg caa ctg acc tct tct gca aag gac ttc aga 48
Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg
1 5 10 15

aac cta gca cta ccc tgg ctc tgc aaa cac ggt tct cta ggt gaa gcc 96
Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala
20 25 30

tct gca gtg att tgc aga agt act cag acg aat gaa cca cag 138
Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

tagttctgct gtttctgagg acgtagttta gagactgaat tcttttgaaa ggacataggg 198
acagttttgca catttgcttg cacatcacac acacacacac acacacacac acacacacac 258
acacacacac acacacacac acacacacac tctctctctc tctctctctc gataccttag 318
gatagggttc taccctgttg ctcaagtaca aagaatcact ctgtggcgga ggcaggcttc 378
aagcttgacg caatcctcct gcaccagttt cctgagtgcc agacttccag gtgtaagcta 438
tggcacttag cagaacacta gctgaatcaa tgaagacact gaggttccaa gagggaaacct 498
gaattatgaa ggtgagtcag aatccagatt tcttggtctt accactctta acctgtatct 558
gttagacccc aagctctgag ctcatagaca agctaattta aaatgctttt taataagcag 618
aaggctcagt tagtacgggg ttcaggatac tgcttactgg caatatttga ctagcctcta 678
ttttgtttgt tttttaaagg cctactgact gtagtgtaat ttgtaggaaa catgttgcta 738
tgtataccca tttaggggta ataaaaatgt tggtaatatt cagccagcac tttccaggta 798
tttccctttt tatccttcat 818

<210> 5

<211> 46

<212> PRT

<213> Mus musculus

<400> 5

Ser Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg
1 5 10 15
Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala
20 25 30
Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

<210> 6

<211> 1753

<212> DNA

<213> Mus musculus

<400> 6

gttttagtaa ccagaggccg caagaagaga tcacttgat atacacgggc cccatctttt 60
gctttttaag acaaaagaaa aagaatcttc ttcaacaagt aagtaaagtc atttactatt 120
tatcatgcta tgggacacct tagtagaaca cgctatctcc agccttatca tatgcatatt 180
ttgttgttgt tggtgttgtt gttgttaaag acagggtctc atatatgcca ggctgggtccc 240
aaactttcag tgtaacccaa gataatctgg aactcccgac tctctgtctc ccacctctcc 300
agtgcaggac actgtttata ccgtgctggg gaattgaact cagagcaccc tgcattgtcag 360
ctaagcattc taccgaccaa gtcccatgcc cagtccttaa ctccccaact tcaactgctt 420
ttaaacatac atacaatcat aacttgccct cagagcagtc tctgtgggtc tcttattctc 480
aaggctgagg cattccaaca ctgttagaaa aacaccatca ggattctttt gtgtttccta 540
gatgcaaaaa tttttgtagg gcgaagtga ggtttttcta atcaagaaaa tgccggtaac 600
aagtctcttc aagctaactg gttggctaag gggatctctt ccaaaagaag agatccacat 660
gtcaggccag ttgtaggcat gatgtcaggt ctccctccct ttctttcttt ctttcttttt 720
ttctttcttt ctttttttct ttctttctta ctttcttact ttctttcttt tctgtttttt 780
ggtttttcga gacagggttt ctttgtatag ccctggctgt cctggaactc gctctgtaga 840
ccaggctggc ctccaactca gaaatctgcc tctgccttta cctcctgagt gctgggaatt 900

```

aaaggtgtgc accaccatgc ccggctggga tgtcattcgt tttcatttct caattttgat 960
acttttatgga agaaaaaaga aaagatagac aagcctcttc atgtaatacc ccatagtctc 1020
aataagtggg gttcgtaacg tggctttctt ttccttacct tttactggta gattttctcg 1080
ttgattgatg tccctgtagg acttactggg tttaagattc ttgggtttcct gttttaagat 1140
ataaagaaac catttcctaa ctaaaacact gccttggaca aatatacttt tggcagtcac 1200
tctgtgtcca gaatggaatt taagctttca tggcctagct gctagtgaag gttctttgct 1260
tttttttggc tgttgtatgt gaaatggggg tgggtgggaa ccacctcact gtgttctagt 1320
gttagtccac ccacccccgc aagcagaatc cttttaccca gctttttcac ccagctgtgc 1380
tcacccgggtg ctacagaacag gcctggacaa gtcacctccc ctagagttct ggggaccttt 1440
gagttgccct catggccaca ccctgattca gaactctcac tctgtcgtaa gatagagcta 1500
ctggggagtt ttatacctca atagactctt actagtttct ctttttcagg ttgtgaaact 1560
caaccttcaa agacactctg ttccattttct gtggactaat aggatcatct ttagcatctg 1620
ccgggtggat gccatccagg cttctttttc tacatctctg tttctcgatt tttgtgagcc 1680
taggaggtgc ctaagctcca ttggctctag attcctggct ttcccatca tgttctccaa 1740
agcatctgaa gct 1753

```

<210> 7
 <211> 158
 <212> DNA
 <213> Mus musculus

```

<400> 7
tgtccaggca gagctagtgg ctgcccctag cgcttcctct tctttgatac cccaaagtct 60
gagtttatta cacatccttg gtgaccaaact cacatggag cttcctccga ggtcttagta 120
aagggaagtt ggaaagggga aattcctgcc ccctgcc 158

```

<210> 8
 <211> 1398
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (249)...(848)

```

<400> 8
gagttttata cctcaataga ctcttactag tttctctttt tcaggttgtg aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
tggatgccat ccaggcttct tttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
          1             5             10

```

```

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
  15             20             25             30

```

```

ctt tca caa gtg tct tca gct gac ttc tct acc ccc aac ata act gag 386
Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
          35             40             45

```

```

tct gga aac cca tct gca gac act aaa agg att acc tgc ttt gct tcc 434
Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser
          50             55             60

```

```

ggg ggt ttc cca aag cct cgc ttc tct tgg tgg gaa aat gga aga gaa 482
Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu
          65             70             75

```

```

tta cct ggc atc aat acg aca att tcc cag gat cct gaa tct gaa ttg 530

```

Leu	Pro	Gly	Ile	Asn	Thr	Thr	Ile	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu		
	80						85				90						
tac	acc	att	agt	agc	caa	cta	gat	ttc	aat	acg	act	cgc	aac	cac	acc	578	
Tyr	Thr	Ile	Ser	Ser	Gln	Leu	Asp	Phe	Asn	Thr	Thr	Arg	Asn	His	Thr		
	95				100				105						110		
att	aag	tgt	ctc	att	aaa	tat	gga	gat	gct	cac	gtg	tca	gag	gac	ttc	626	
Ile	Lys	Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe		
				115				120						125			
acc	tgg	gaa	aaa	ccc	cca	gaa	gac	cct	cct	gat	agc	aag	aac	aca	ctt	674	
Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu		
			130					135					140				
gtg	ctc	ttt	ggg	gca	gga	ttc	ggc	gca	gta	ata	aca	gtc	gtc	gtc	atc	722	
Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile		
		145					150					155					
gtt	gtc	atc	atc	aaa	tgc	ttc	tgt	aag	cac	aga	agc	tgt	ttc	aga	aga	770	
Val	Val	Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg		
	160					165					170						
aat	gag	gca	agc	aga	gaa	aca	aac	aac	agc	ctt	acc	ttc	ggg	cct	gaa	818	
Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu		
	175				180					185					190		
gaa	gca	tta	gct	gaa	cag	acc	gtc	ttc	ctt	tagttcttct	ctgtccatgt					868	
Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu								
				195				200									

gggatacatg gtattatgtg gctcatgagg tacaatcttt ctttcagcac cgtgctagct 928
gatctttcgg acaacttgac acaagataga gttaactggg aagagaaagc cttgaatgag 988
gatttctttc catcaggaag ctacgggcaa gtttgctggg cctttgattg cttgatgact 1048
gaagtggaaa ggctgagccc actgtgggtg gtgctagccc tgggcagggg cagggtgaccc 1108
tgggtggtat aagaaaaaga gctgtcacta aaaggagagg tgcctagtct tactgcaact 1168
tgatatgtca tgtttggttg gtgtctgtgg gaggcctgcc cttttctgaa gagaagtggg 1228
gggagagtgg atgggggtggg ggcagaggaa aagtggggga gagggcctgg gaggagagga 1288
gggaggggga cggggtgggg gtgggggaaaa ctatggttgg gatgtaaaaa cggataataa 1348
tataaatatt aaataaaaaag agagtattga gcaaaaaaaa aaaaaaaaaa 1398

<210> 9
<211> 200
<212> PRT
<213> Mus musculus

<400> 9

Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu	Lys	Phe
1				5					10					15	
Pro	Cys	Pro	Arg	Leu	Ile	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	Leu	Ser
			20					25					30		
Gln	Val	Ser	Ser	Ala	Asp	Phe	Ser	Thr	Pro	Asn	Ile	Thr	Glu	Ser	Gly
		35					40					45			
Asn	Pro	Ser	Ala	Asp	Thr	Lys	Arg	Ile	Thr	Cys	Phe	Ala	Ser	Gly	Gly
	50					55				60					
Phe	Pro	Lys	Pro	Arg	Phe	Ser	Trp	Leu	Glu	Asn	Gly	Arg	Glu	Leu	Pro
65					70				75						80
Gly	Ile	Asn	Thr	Thr	Ile	Ser	Gln	Asp	Pro	Glu	Ser	Glu	Leu	Tyr	Thr
			85					90						95	
Ile	Ser	Ser	Gln	Leu	Asp	Phe	Asn	Thr	Arg	Asn	His	Thr	Ile	Lys	
			100					105					110		

Cys	Leu	Ile	Lys	Tyr	Gly	Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp
		115					120					125			
Glu	Lys	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu
	130					135					140				
Phe	Gly	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val
145					150					155					160
Ile	Ile	Lys	Cys	Phe	Cys	Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu
			165						170					175	
Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala
			180					185					190		
Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu								
		195					200								

<210> 10
 <211> 1570
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (249)...(890)

<400> 10
 gagttttata cctcaataga ctcttactag tttctctttt tcaggttggtg aaactcaacc 60
 ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
 tggatgccat ccaggcttct tttctacat ctctgtttct cgatttttgt gagcctagga 180
 ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
 ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30

ctt tca caa gtg tct tca gct gac ttc tct acc ccc aac ata act gag 386
 Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
 35 40 45

tct gga aac cca tct gca gac act aaa agg att acc tgc ttt gct tcc 434
 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser
 50 55 60

ggg ggt ttc cca aag cct cgc ttc tct tgg ttg gaa aat gga aga gaa 482
 Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu
 65 70 75

tta cct ggc atc aat acg aca att tcc cag gat cct gaa tct gaa ttg 530
 Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu
 80 85 90

tac acc att agt agc caa cta gat ttc aat acg act cgc aac cac acc 578
 Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr
 95 100 105 110

att aag tgt ctc att aaa tat gga gat gct cac gtg tca gag gac ttc 626
 Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe
 115 120 125

acc tgg gaa aaa ccc cca gaa gac cct cct gat agc aag aac aca ctt 674

Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu
 130 135 140

gtg ctc ttt ggg gca gga ttc ggc gca gta ata aca gtc gtc gtc atc 722
 Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile
 145 150 155

gtt gtc atc atc aaa tgc ttc tgt aag cac ggt ctc atc tac cat ttg 770
 Val Val Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu
 160 165 170

caa ctg acc tct tct gca aag gac ttc aga aac cta gca cta ccc tgg 818
 Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp
 175 180 185 190

ctc tgc aaa cac ggt tct cta ggt gaa gcc tct gca gtg att tgc aga 866
 Leu Cys Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg
 195 200 205

agt act cag acg aat gaa cca cag tagttctgct gtttctgagg acgtagtttta 920
 Ser Thr Gln Thr Asn Glu Pro Gln
 210

gagactgaat tcttttgaaa ggacataggg acagtttgca catttgcttg cacatcacac 980
 acacacacac acacacacac acacacacac acacacacac acacacacac acacacacac 1040
 tctctctctc tctctctctc gataccttag gataggggtc taccctgttg ctcagtgaac 1100
 aagaatcact ctgtggcgga ggcaggcttc aagcttgacag caatcctcct gcaccagttt 1160
 cctgagtgcc agacttccag gtgtaagcta tggcacttag cagaacacta gctgaatcaa 1220
 tgaagacact gaggttccaa gagggaaacct gaattatgaa ggtgagtcag aatccagatt 1280
 tcttggtctt accactctta acctgtatct gttagacccc aagctctgag ctcatagaca 1340
 agctaattta aaatgctttt taataagcag aaggctcagt tagtacgggg ttcaggatac 1400
 tgcttactgg caatatattga ctagcctcta ttttggttgt tttttaaagg cctactgact 1460
 gtagtgaat ttgtaggaaa catgttgcta tgtataccca tttgagggta ataaaaatgt 1520
 tggtaatttt cagccagcac tttccaggta tttccctttt ttccttcat 1570

<210> 11
 <211> 214
 <212> PRT
 <213> Mus musculus

<400> 11

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35 40 45
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50 55 60
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65 70 75 80
 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85 90 95
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys
 100 105 110
 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp
 115 120 125
 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu
 130 135 140
 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val
 145 150 155 160

```

Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu
                165                170                175
Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys
                180                185                190
Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr
                195                200                205
Gln Thr Asn Glu Pro Gln
                210

```

```

<210> 12
<211> 1261
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (194)...(1135)

```

```

<221> misc_feature
<222> 3, 7
<223> n = A,T,C or G

```

```

<400> 12
agncccnaga ttatttctcc ctgtataagg gacgcccagg aggcctgggg agcggacaag 60
gctcctttta cttttcttct tttttatatt tttttacctt ctattttttt cttcatgttc 120
ctgtgatctt cgggaatgct gctgtgcttg tgtgtgtggt ccctgagcgc cgaggtggag 180
aggcactggg gac atg tat gtc atc aag aca tgt gca acc tgc acc atg 229
          Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met
              1              5              10

ggc ttg gca atc ctt atc ttt gtg aca gtc ttg ctg atc tca gat gct 277
Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala
          15              20              25

gtt tcc gtg gag acg caa gct tat ttc aat ggg act gca tat ctg ccg 325
Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro
          30              35              40

tgc cca ttt aca aag gct caa aac ata agc ctg agt gag ctg gta gta 373
Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val
          45              50              55              60

ttt tgg cag gac cag caa aag ttg gtt ctg tac gag cac tat ttg ggc 421
Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly
          65              70              75

aca gag aaa ctt gat agt gtg aat gcc aag tac ctg ggc cgc acg agc 469
Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser
          80              85              90

,
ttt gac agg aac aac tgg act cta cga ctt cac aat gtt cag atc aag 517
Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys
          95              100              105

gac atg ggc tcg tat gat tgt ttt ata caa aaa aag cca ccc aca gga 565
Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly
          110              115              120

tca att atc ctc caa cag aca tta aca gaa ctg tca gtg atc gcc aac 613
Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn

```

125	130	135	140	
ttc agt gaa cct gaa ata aaa ctg gct cag aat gta aca gga aat tct				661
Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser				
	145	150	155	
ggc ata aat ttg acc tgc acg tct aag caa ggt cac ccg aaa cct aag				709
Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys				
	160	165	170	
aag atg tat ttt ctg ata act aat tca act aat gag tat ggt gat aac				757
Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn				
	175	180	185	
atg cag ata tca caa gat aat gtc aca gaa ctg ttc agt atc tcc aac				805
Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn				
	190	195	200	
agc ctc tct ctt tca ttc ccg gat ggt gtg tgg cat atg acc gtt gtg				853
Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val				
	205	210	215	220
tgt gtt ctg gaa acg gag tca atg aag att tcc tcc aaa cct ctc aat				901
Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn				
	225	230	235	
ttc act caa gag ttt cca tct cct caa acg tat tgg aag gag att aca				949
Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr				
	240	245	250	
gct tca gtt act gtg gcc ctc ctc ctt gtg atg ctg ctc atc att gta				997
Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile Val				
	255	260	265	
tgt cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc tct				1045
Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser				
	270	275	280	
aag tta gag cgg gat agt aac gct gac aga gag act atc aac ctg aag				1093
Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys				
	285	290	295	300
gaa ctt gaa ccc caa att gct tca gca aaa cca aat gca gag				1135
Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu				
	305	310		
tgaaggcagt gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc				1195
agagtttctc agaattcaaaa aatgttctca gctgattgga attctacagt tgaataatta				1255
aagaac				1261

<210> 13

<211> 314

<212> PRT

<213> Mus musculus

<400> 13

Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met Gly Leu Ala Ile

1

5

10

15

Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu

20

25

30

Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr

<212> PRT

<213> Mus musculus

<400> 15

Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
1 5 10

<210> 16

<211> 1716

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(1166)

<400> 16

gagttttata cctcaataga ctcttactag tttctctttt tcaggttgtg aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catcttttagc atctgccggg 120
tggatgccat ccaggcttct ttttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggttttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
1 5 10

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
15 20 25 30

ctt tca caa gtg tct tca gat gtt gat gaa caa ctg tcc aag tca gtg 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
35 40 45

aaa gat aag gta ttg ctg cct tgc cgt tac aac tct cct cat gaa gat 434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
50 55 60

gag tct gaa gac cga atc tac tgg caa aaa cat gac aaa gtg gtg ctg 482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
65 70 75

tct gtc att gct ggg aaa cta aaa gtg tgg ccc gag tat aag aac cgg 530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
80 85 90

act tta tat gac aac act acc tac tct ctt atc atc ctg ggc ctg gtc 578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
95 100 105 110

ctt tca gac cgg ggc aca tac agc tgt gtc gtt caa aag aag gaa aga 626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
115 120 125

gga acg tat gaa gtt aaa cac ttg gct tta gta aag ttg tcc atc aaa 674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
130 135 140

gct gac ttc tct acc ccc aac ata act gag tct gga aac cca tct gca 722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
145 150 155

gac act aaa agg att acc tgc ttt gct tcc ggg ggt ttc cca aag cct 770
 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
 160 165 170

cgc ttc tct tgg ttg gaa aat gga aga gaa tta cct ggc atc aat acg 818
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
 175 180 185 190

aca att tcc cag gat cct gaa tct gaa ttg tac acc att agt agc caa 866
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
 195 200 205

cta gat ttc aat acg act cgc aac cac acc att aag tgt ctc att aaa 914
 Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
 210 215 220

tat gga gat gct cac gtg tca gag gac ttc acc tgg gaa aaa ccc cca 962
 Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
 225 230 235

gaa gac cct cct gat agc aag aac aca ctt gtg ctc ttt ggg gca gga 1010
 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
 240 245 250

ttc ggc gca gta ata aca gtc gtc gtc atc gtt gtc atc atc aaa tgc 1058
 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
 255 260 265 270

ttc tgt aag cac aga agc tgt ttc aga aga aat gag gca agc aga gaa 1106
 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
 275 280 285

aca aac aac agc ctt acc ttc ggg cct gaa gaa gca tta gct gaa cag 1154
 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
 290 295 300

acc gtc ttc ctt tagttcttct ctgtccatgt gggatacatg gtattatgtg 1206
 Thr Val Phe Leu
 305

gctcatgagg tacaatcttt ctttcagcac cgtgctagct gatctttcgg acaacttgac 1266
 acaagataga gttaactggg aagagaaagc cttgaatgag gatttctttc catcaggaag 1326
 ctacgggcaa gtttgctggg cctttgattg cttgatgact gaagtggaaa ggctgagccc 1386
 actgtgggtg gtgctagccc tgggcagggg caggtgaccc tgggtggtat aagaaaaaga 1446
 gctgtcacta aaaggagagg tgcttagtct tactgcaact tgatatgtca tgtttggttg 1506
 gtgtctgtgg gaggcctgcc cttttctgaa gagaagtggg gggagagtgg atgggggtggg 1566
 ggagagaggaa aagtggggga gagggcctgg gaggagagga gggaggggga cgggggtggg 1626
 gtggggaaaa ctatggttg gatgtaaaaa cggataataa tataaatatt aaataaaaaag 1686
 agagtattga gcaaaaaaaaa aaaaaaaaaa 1716

<210> 17
 <211> 306
 <212> PRT
 <213> Mus musculus

<400> 17
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110
 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 130 135 140
 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 145 150 155 160
 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 165 170 175
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 180 185 190
 Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
 195 200 205
 Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
 210 215 220
 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
 225 230 235 240
 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
 245 250 255
 Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
 260 265 270
 Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
 275 280 285
 Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
 290 295 300
 Phe Leu
 305

<210> 18
 <211> 1491
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (318)...(1181)

<400> 18
 ccaaagaaaa agtgatttgt cattgcttta tagactgtaa gaagagaaca tctcagaagt 60
 ggagtcttac cctgaaatca aaggatttaa agaaaaagtg gaatttttct tcagcaagct 120
 gtgaaactaa atccacaacc tttggagacc caggaacacc ctccaatctc tgttgtgttt 180
 gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcagc cctgcctggt 240
 ttgcacctgg gaagtgcct ggtcttactt gggtccaaat tggtggcttt cacttttgac 300
 cctaagcatc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 tcc aag tgt cca tac ctg aat ttc ttt cag ctc ttg gtg ctg gct ggt 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25

ctt tct cac ttc tgt tca ggt gtt atc cac gtg acc aag gaa gtg aaa	446
Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys	
30 35 40	
gaa gtg gca acg ctg tcc tgt ggt cac aat gtt tct gtt gaa gag ctg	494
Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu	
45 50 55	
gca caa act cgc atc tac tgg caa aag gag aag aaa atg gtg ctg act	542
Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr	
60 65 70 75	
atg atg tct ggg gac atg aat ata tgg ccc gag tac aag aac cgg acc	590
Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr	
80 85 90	
atc ttt gat atc act aat aac ctc tcc att gtg atc ctg gct ctg cgc	638
Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg	
95 100 105	
cca tct gac gag ggc aca tac gag tgt gtt gtt ctg aag tat gaa aaa	686
Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys	
110 115 120	
gac gct ttc aag cgg gaa cac ctg gct gaa gtg acg tta tca gtc aaa	734
Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys	
125 130 135	
gct gac ttc cct aca cct agt ata tct gac ttt gaa att cca act tct	782
Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser	
140 145 150 155	
aat att aga agg ata att tgc tca acc tct gga ggt ttt cca gag cct	830
Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro	
160 165 170	
cac ctc tcc tgg ttg gaa aat gga gaa gaa tta aat gcc atc aac aca	878
His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr	
175 180 185	
aca gtt tcc caa gat cct gaa act gag ctc tat gct gtt agc agc aaa	926
Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys	
190 195 200	
ctg gat ttc aat atg aca acc aac cac agc ttc atg tgt ctc atc aag	974
Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys	
205 210 215	
tat gga cat tta aga gtg aat cag acc ttc aac tgg aat aca acc aag	1022
Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys	
220 225 230 235	
caa gag cat ttt cct gat aac ctg ctc cca tcc tgg gcc att acc tta	1070
Gln Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu	
240 245 250	
atc tca gta aat gga att ttt gtg ata tgc tgc ctg acc tac tgc ttt	1118
Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe	
255 260 265	
gcc cca aga tgc aga gag aga agg agg aat gag aga ttg aga agg gaa	1166

Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu
270 275 280

agt gta cgc cct gta taacagtgtc cgcagaagca aggggctgaa aagatctgaa 1221
Ser Val Arg Pro Val
285

ggtagcctcc gtcattctctt ctgggataca tggatcgtgg ggatcatgag gcattcttcc 1281
cttaacaaat ttaagctgtt ttaccacta cctcaccttc ttaaaaacct ctttcagatt 1341
aagctgaaca gttacaagat ggctggcatc cctctccttt ctcccatat gcaatttgct 1401
taatgtaacc tcttcttttg ccatgtttcc attctgccat cttgaattgt cttgtcagcc 1461
aattcattat ctattaaaca ctaatttgag 1491

<210> 19
<211> 288
<212> PRT
<213> Homo sapiens

<400> 19
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190
Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205
Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220
Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240
Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255
Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270
Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

<210> 20
<211> 1151
<212> DNA
<213> Mus musculus

<220>

<221> CDS

<222> (99) ... (1025)

<400> 20

ggagcaagca gacgcgtaag agtggctcct gtaggcagca cggacttgaa caaccagact 60
cctgtagacg tgttccagaa cttacggaag caccacacg atg gac ccc aga tgc acc 116
Met Asp Pro Arg Cys Thr
1 5

atg ggc ttg gca atc ctt atc ttt gtg aca gtc ttg ctg atc tca gat 164
Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp
10 15 20

gct gtt tcc gtg gag acg caa gct tat ttc aat ggg act gca tat ctg 212
Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu
25 30 35

ccg tgc cca ttt aca aag gct caa aac ata agc ctg agt gag ctg gta 260
Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val
40 45 50

gta ttt tgg cag gac cag caa aag ttg gtt ctg tac gag cac tat ttg 308
Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu
55 60 65 70

ggc aca gag aaa ctt gat agt gtg aat gcc aag tac ctg ggc cgc acg 356
Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr
75 80 85

agc ttt gac agg aac aac tgg act cta cga ctt cac aat gtt cag atc 404
Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile
90 95 100

aag gac atg ggc tgc tat gat tgt ttt ata caa aaa aag cca ccc aca 452
Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr
105 110 115

gga tca att atc ctc caa cag aca tta aca gaa ctg tca gtg atc gcc 500
Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala
120 125 130

aac ttc agt gaa cct gaa ata aaa ctg gct cag aat gta aca gga aat 548
Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn
135 140 145 150

tct ggc ata aat ttg acc tgc acg tct aag caa ggt cac ccg aaa cct 596
Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro
155 160 165

aag aag atg tat ttt ctg ata act aat tca act aat gag tat ggt gat 644
Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp
170 175 180

aac atg cag ata tca caa gat aat gtc aca gaa ctg ttc agt atc tcc 692
Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser
185 190 195

aac agc ctc tct ctt tca ttc ccg gat ggt gtg tgg cat atg acc gtt 740
Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val

200	205	210	
gtg tgt gtt ctg gaa acg gag tca atg aag att tcc tcc aaa cct ctc			788
Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu			
215	220	225	230
aat ttc act caa gag ttt cca tct cct caa acg tat tgg aag gag att			836
Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile			
235	240		245
aca gct tca gtt act gtg gcc ctc ctc ctt gtg atg ctg ctc atc att			884
Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile			
250	255		260
gta tgt cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc			932
Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala			
265	270		275
tct aag tta gag cgg gat agt aac gct gac aga gag act atc aac ctg			980
Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu			
280	285		290
aag gaa ctt gaa ccc caa att gct tca gca aaa cca aat gca gag			1025
Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu			
295	300	305	
tgaaggcagt gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc			1085
agagttttctc agaattcaaaa aatgtttctca gctgattgga attctacagt tgaataatta			1145
aagaac			1151
<210> 21			
<211> 309			
<212> PRT			
<213> Mus musculus			
<400> 21			
Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr			
1 5 10 15			
Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe			
20 25 30			
Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile			
35 40 45			
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val			
50 55 60			
Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala			
65 70 75 80			
Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg			
85 90 95			
Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile			
100 105 110			
Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr			
115 120 125			
Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala			
130 135 140			
Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys			
145 150 155 160			
Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser			
165 170 175			
Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr			
180 185 190			
Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly			

195	200	205
Val Trp His Met Thr	Val Val Cys Val Leu Glu Thr	Glu Ser Met Lys
210	215	220
Ile Ser Ser Lys Pro	Leu Asn Phe Thr Gln Glu Phe	Pro Ser Pro Gln
225	230	235
Thr Tyr Trp Lys Glu	Ile Thr Ala Ser Val Thr Val	Ala Leu Leu Leu
245	250	255
Val Met Leu Leu Ile	Ile Val Cys His Lys Lys	Pro Asn Gln Pro Ser
260	265	270
Arg Pro Ser Asn Thr	Ala Ser Lys Leu Glu Arg	Asp Ser Asn Ala Asp
275	280	285
Arg Glu Thr Ile Asn	Leu Lys Glu Leu Glu	Pro Gln Ile Ala Ser Ala
290	295	300
Lys Pro Asn Ala Glu		
305		

<210> 22
 <211> 1120
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)...(1093)

<400> 22
 cacagggtga aagctttgct tctctgctgc tgtaacaggg actagcacag acacacggat 60
 gagtgggggtc atttccagat attaggtcac agcagaagca gccaaa atg gat ccc 115
 Met Asp Pro
 1

cag tgc act atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg 163
 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
 5 10 15

ctc tct ggt gct gct cct ctg aag att caa gct tat ttc aat gag act 211
 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
 20 25 30 35

gca gac ctg cca tgc caa ttt gca aac tct caa aac caa agc ctg agt 259
 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
 40 45 50

gag cta gta gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag 307
 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
 55 60 65

gta tac tta ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg 355
 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
 70 75 80

ggc cgc aca agt ttt gat tgc gac agt tgg acc ctg aga ctt cac aat 403
 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
 85 90 95

ctt cag atc aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa 451
 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
 100 105 110 115

aag ccc aca gga atg att cgc atc cac cag atg aat tct gaa ctg tca 499

Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser		
				120					125					130			
gtg	ctt	gct	aac	ttc	agt	caa	cct	gaa	ata	gta	cca	att	tct	aat	ata	547	
Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile		
			135					140					145				
aca	gaa	aat	gtg	tac	ata	aat	ttg	acc	tgc	tca	tct	ata	cac	ggg	tac	595	
Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr		
		150					155					160					
cca	gaa	cct	aag	aag	atg	agt	gtt	ttg	cta	aga	acc	aag	aat	tca	act	643	
Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr		
	165					170					175						
atc	gag	tat	gat	ggg	att	atg	cag	aaa	tct	caa	gat	aat	gtc	aca	gaa	691	
Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu		
180					185				190						195		
ctg	tac	gac	gtt	tcc	atc	agc	ttg	tct	gtt	tca	ttc	cct	gat	gtt	acg	739	
Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr		
				200					205					210			
agc	aat	atg	acc	atc	ttc	tgt	att	ctg	gaa	act	gac	aag	acg	cgg	ctt	787	
Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu		
			215					220					225				
tta	tct	tca	cct	ttc	tct	ata	gag	ctt	gag	gac	cct	cag	cct	ccc	cca	835	
Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro		
			230				235					240					
gac	cac	att	cct	tgg	att	aca	gct	gta	ctt	cca	aca	gtt	att	ata	tgt	883	
Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys		
	245					250					255						
gtg	atg	gtt	ttc	tgt	cta	att	cta	tgg	aaa	tgg	aag	aag	aag	aag	cgg	931	
Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg		
260					265			270							275		
cct	cgc	aac	tct	tat	aaa	tgt	gga	acc	aac	aca	atg	gag	agg	gaa	gag	979	
Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu		
				280				285						290			
agt	gaa	cag	acc	aag	aaa	aga	gaa	aaa	atc	cat	ata	cct	gaa	aga	tct	1027	
Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser		
			295					300					305				
gat	gaa	gcc	cag	cgt	gtt	ttt	aaa	agt	tcg	aag	aca	tct	tca	tgc	gac	1075	
Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp		
		310					315					320					
aaa	agt	gat	aca	tgt	ttt	taattaaaga	gtaaagccca	aaaaaaaa								1120	
Lys	Ser	Asp	Thr	Cys	Phe												
			325														

<210> 23
 <211> 329
 <212> PRT
 <213> Homo sapiens

<400> 23

```

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1      5      10      15
Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20      25      30
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35      40      45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50      55      60
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65      70      75      80
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85      90      95
Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100     105     110
His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115     120     125
Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130     135     140
Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145     150     155     160
His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165     170     175
Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180     185     190
Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195     200     205
Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210     215     220
Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225     230     235     240
Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245     250     255
Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260     265     270
Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275     280     285
Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290     295     300
Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305     310     315     320
Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

```

<210> 24

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (148)...(1134)

<400> 24

```

aggagcctta ggaggtacgg ggagctcgca aatactcctt ttggtttatt cttaccacct 60
tgcttctgtg ttccttgga atgctgctgt gcttatgcat ctggtctctt tttggagcta 120
cagtggacag gcatttgtga cagcaact atg gat ccc cag tgc act atg gga ctg 174
Met Asp Pro Gln Cys Thr Met Gly Leu
1      5

```

agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt gct gct cct	222
Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala Pro	
10 15 20 25	
ctg aag att caa gct tat ttc aat gag act gca gac ctg cca tgc caa	270
Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys Gln	
30 35 40	
ttt gca aac tct caa aac caa agc ctg agt gag cta gta gta ttt tgg	318
Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val Val Phe Trp	
45 50 55	
cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta ggc aaa gag	366
Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu Gly Lys Glu	
60 65 70	
aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca agt ttt gat	414
Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr Ser Phe Asp	
75 80 85	
tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc aag gac aag	462
Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile Lys Asp Lys	
90 95 100 105	
ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca gga atg att	510
Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr Gly Met Ile	
110 115 120	
cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct aac ttc agt	558
Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala Asn Phe Ser	
125 130 135	
caa cct gaa ata gta cca att tct aat ata aca gaa aat gtg tac ata	606
Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn Val Tyr Ile	
140 145 150	
aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct aag aag atg	654
Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro Lys Lys Met	
155 160 165	
agt gtt ttg cta aga acc aag aat tca act atc gag tat gat ggt att	702
Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp Gly Ile	
170 175 180 185	
atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac gtt tcc atc	750
Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp Val Ser Ile	
190 195 200	
agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg acc atc ttc	798
Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met Thr Ile Phe	
205 210 215	
tgt att ctg gaa act gac aag acg cgg ctt tta tct tca cct ttc tct	846
Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser Pro Phe Ser	
220 225 230	
ata gag ctt gag gac cct cag cct ccc cca gac cac att cct tgg att	894
Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile Pro Trp Ile	
235 240 245	
aca gct gta ctt cca aca gtt att ata tgt gtg atg gtt ttc tgt cta	942

Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	
250					255					260					265	
att cta tgg aaa tgg aag aag aag aag cgg cct cgc aac tct tat aaa 990																
Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	
			270						275					280		
tgt gga acc aac aca atg gag agg gaa gag agt gaa cag acc aag aaa 1038																
Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	
			285					290					295			
aga gaa aaa atc cat ata cct gaa aga tct gat gaa gcc cag cgt gtt 1086																
Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	
		300					305					310				
ttt aaa agt tgc aag aca tct tca tgc gac aaa agt gat aca tgt ttt 1134																
Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys	Phe	
	315					320					325					
taattaaaga gtaaagccca aaaaaaa 1161																

<210> 25
 <211> 629
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(96)

<400> 25																
aga	agc	tgt	ttc	aga	aga	aat	gag	gca	agc	aga	gaa	aca	aac	aac	agc	48
Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	
1				5				10					15			
ctt acc ttc ggg cct gaa gaa gca tta gct gaa cag acc gtc ttc ctt 96																
Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu	
			20					25					30			

tagttcttct	ctgtccatgt	gggatacatg	gtattatgtg	gctcatgagg	tacaatcttt	156
ctttcagcac	cgtgctagct	gatctttcgg	acaacttgac	acaagataga	gttaactggg	216
aagagaaagc	cttgaatgag	gatttctttc	catcaggaag	ctacgggcaa	gtttgctggg	276
cctttgattg	cttgatgact	gaagtggaaa	ggctgagccc	actgtgggtg	gtgctagaaa	336
tgggcagggg	caggtgaccc	tgggtggtat	aagaaaaaga	gctgtcacta	aaaggagagg	396
tgcttagtct	tactgcaact	tgatatgtca	tgtttggttg	gtgtctgtgg	gaggcctgcc	456
cttttctgaa	gagaagtgg	gggagagtgg	atggggtggg	ggcagaggaa	aagtggggga	516
gagggcctgg	gaggagagga	gggaggggga	cggggtgggg	gtggggaaaa	ctatggttgg	576
gatgtaaaaa	cggataataa	tataaatatt	aaataaaaaag	agagtattga	gca	629

<210> 26
 <211> 32
 <212> PRT
 <213> Mus musculus

<400> 26																
Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn	Asn	Ser	
1				5				10					15			
Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val	Phe	Leu	
			20					25					30			

<210> 27
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(69)

<400> 27
 tgc ttt gcc cca aga tgc aga gag aga agg agg aat gag aga ttg aga 48
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 agg gaa agt gta cgc cct gta taacagtgtc cgcagaagca aggggctgaa 99
 Arg Glu Ser Val Arg Pro Val
 20
 aagatctgaa ggtagcctcc gtcattctctt ctgggataca tggatcgtgg ggatcatgag 159
 gcattcttcc cttaacaaat ttaagctggt ttaccacta cctcaccttc ttaaaaacct 219
 ctttcagatt aagctgaaca gttacaagat ggctggcatc cctctccttt ctccccatat 279
 gcaatttgct taatgtaacc ttttcttttg ccatgtttcc attctgccat cttgaattgt 339
 cttgtcagcc aattcattat ctattaaaca ctaatttgag 379

<210> 28
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 28
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 Arg Glu Ser Val Arg Pro Val
 20

<210> 29
 <211> 261
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(135)

<400> 29
 cac aag aag ccg aat cag cct agc agg ccc agc aac aca gcc tct aag 48
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15
 tta gag cgg gat agt aac gct gac aga gag act atc aac ctg aag gaa 96
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30
 ctt gaa ccc caa att gct tca gca aaa cca aat gca gag tgaaggcagt 145
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45
 gagagcctga ggaaagagtt aaaaattgct ttgcctgaaa taagaagtgc agagttttctc 205
 agaattcaaa aatgtttctca gctgattgga attctacagt tgaataatta aagaac 261

<210> 30
 <211> 45
 <212> PRT
 <213> Mus musculus

<400> 30
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45

<210> 31
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(183)

<400> 31
 aaa tgg aag aag aag aag cgg cct cgc aac tct tat aaa tgt gga acc 48
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15
 aac aca atg gag agg gaa gag agt gaa cag acc aag aaa aga gaa aaa 96
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30
 atc cat ata cct gaa aga tct gat gaa gcc cag cgt gtt ttt aaa agt 144
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45
 tcg aag aca tct tca tgc gac aaa agt gat aca tgt ttt taattaaaga 193
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60
 gtaaagccca aaaaaaa 210

<210> 32
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 32
 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30
 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60

<210> 33
 <211> 359
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249)...(359)

<400> 33

```

gagttttata cctcaataga ctcttactag tttctctttt tcaggttggt aaactcaacc 60
ttcaaagaca ctctgttcca tttctgtgga ctaataggat catctttagc atctgccggg 120
tggaatgccat ccaggcttct tttctacat ctctgtttct cgatttttgt gagcctagga 180
ggtgcctaag ctccattggc tctagattcc tggctttccc catcatgttc tccaaagcat 240
ctgaagct atg gct tgc aat tgt cag ttg atg cag gat aca cca ctc ctc 290
      Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
        1             5             10

```

```

aag ttt cca tgt cca agg ctc aat ctt ctc ttt gtg ctg ctg att cgt 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
  15             20             25             30

```

```

ctt tca caa gtg tct tca gat 359
Leu Ser Gln Val Ser Ser Asp
          35

```

<210> 34

<211> 37

<212> PRT

<213> Mus musculus

<400> 34

```

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
  1             5             10             15
Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
          20             25             30
Gln Val Ser Ser Asp
      35

```

<210> 35

<211> 416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (318)...(416)

<400> 35

```

ccaaagaaaa agtgatttgt cattgcttta tagactgtaa gaagagaaca tctcagaagt 60
ggagtctttac cctgaaatca aaggatttaa agaaaaagtg gaatttttct tcagcaagct 120
gtgaaactaa atccacaacc ttggagacc caggaacacc ctccaatctc tgtgtgtttt 180
gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcagc cctgcctggt 240
ttgcacctgg gaagtgcctt ggtcttactt gggtcctaat tggtggcttt cacttttgac 300
cctaagcatc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
      Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
        1             5             10

```

```

tcc aag tgt cca tac ctg aat ttc ttt cag ctc ttg gtg ctg gct ggt 398
Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
      15             20             25

```

ctt tct cac ttc tgt tca
 Leu Ser His Phe Cys Ser
 30

416

<210> 36
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 Ser

<210> 37
 <211> 113
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (99)...(113)

<400> 37
 ggagcaagca gacgcgtaag agtggctcct gtaggcagca cggacttgaa caaccagact 60
 cctgtagacg tggtccagaa cttacggaag caccacag atg gac ccc aga tgc 113
 Met Asp Pro Arg Cys
 1 5

<210> 38
 <211> 5
 <212> PRT
 <213> Mus musculus

<400> 38
 Met Asp Pro Arg Cys
 1 5

<210> 39
 <211> 124
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)...(124)

<400> 39
 cacagggtga aagctttgct tctctgctgc tgtaacaggg actagcacag acacacggat 60
 gagtgggggtc atttccagat attaggtcac agcagaagca gccaaa atg gat ccc 115
 Met Asp Pro
 1

cag tgc act
Gln Cys Thr
5

124

<210> 40
<211> 6
<212> PRT
<213> Homo sapiens

<400> 40
Met Asp Pro Gln Cys Thr
1 5

<210> 41
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (148)...(195)

<400> 41
aggagcctta ggaggtacgg ggagctcgca aatactcctt ttggtttatt cttaccacct 60
tgcttctgtg ttccttggga atgctgctgt gcttatgcat ctggctctctt tttggagcta 120
cagtggacag gcatttgtga cagcaact atg gga ctg agt aac att ctc ttt gtg 174
Met Gly Leu Ser Asn Ile Leu Phe Val
1 5

atg gcc ttc ctg ctc tct ggt 195
Met Ala Phe Leu Leu Ser Gly
10 15

<210> 42
<211> 16
<212> PRT
<213> Homo sapiens

<400> 42
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15